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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/155,676DATE: 02/29/2000
TIME: 01:54:05

INPUT SET: S34879.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: WALLACH, David
MALININ, Nikolai
BOLDIN, Mark
KOVALENKO, Andrei
METT, Igor

(ii) TITLE OF INVENTION: MODULATORS OF TNF RECEPTOR ASSOCIATED
FACTOR (TRAF), THEIR PREPARATION AND USE

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
(B) STREET: 624 Ninth Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/155,676
(B) FILING DATE: 04-JAN-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/IL97/00117
(B) FILING DATE: 01-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 117800
(B) FILING DATE: 02-APR-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 119133
(B) FILING DATE: 26-AUG-1996

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47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: BROWDY, Roger L.
49 (B) REGISTRATION NUMBER: 25,618
50 (C) REFERENCE/DOCKET NUMBER: WALLACH=21
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 202-628-5197
54 (B) TELEFAX: 202-737-3528
55
56
57 (2) INFORMATION FOR SEQ ID NO: 1:
58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 1906 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64
65 (ii) MOLECULE TYPE: cDNA
66
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68
69 CATTGGGTCA CGCGGTGGCG GCGCTCTAGA ATAGTGGATC CCCCAGGGCTG CAGGAATTCG 60
70
71 ATTCGAGGCC ACGAAGGCCG GCGGCGCGGC GCANGCACCG GCCCGGGGAN AGGCNCCATG 120
72
73 AGCGGATCNC NGAACNATGA CAAAAGACAA TTTCTGCTGG AGCGACTGCT GGATGCAGTG 180
74
75 AAACAGTGCC AGATCCGCTT TNGAGGGAGA AAGGAGATTG CCTCGGATTC CGACAGCAGG 240
76
77 GTCACCTGTC TGTGTGCCCA GTTTGAAGCC GTCCTGCAGC ATGGCTTGAA GAGGAGTCGA 300
78
79 GGATTGGCAC TCACAGCGGC AGCGATCAAG CAGGCAGCGG GCTTTGCCAG CAAAACCGAA 360
80
81 ACAGAGCCCG TGTTCTGGTA CTACGTGAAG GAGGTCTCTA ACAAGCACGA GCTGCAGCGC 420
82
83 TTCTACTCCC TGCGCCACAT CGCCTCAGAC GTGGGCCGGG GTCGCGCCTG GCTGCGCTGT 480
84
85 GCCCTCAACG AACACTCCCT GGAGCGCTAC CTGCACATGC TCCTGGCCGA CCGCTGCAGG 540
86
87 CTGAGCACTT TTTATGAAGA CTGGTCTTTT GTGATGGATG AAGAAAGGTC CAGTATGCTT 600
88
89 CCTACCATGG CAGCAGGTCT GAACTCCATA CTCTTTGCGA TTAACATCGA CAACAAGGAT 660
90
91 TTGAACGGGC AGAGTAAGTT TGCTCCCACC GTTTCAGACC TCTTAAAGGA GTCAACGCAG 720
92
93 AACGTGACCT CTTTGCTGAA GGAGTCCACG CAAGGAGTGA GCAGCCTGTT CAGGGAGATC 780
94
95 ACAGCCTCCT CTGCCGTCTC CATCCTCATC AAACCTGAAC AGGAGACCGA CCCTTGCCCTG 840
96
97 TCGTGTCCAG GAATGTCAGT GCTGATGCCA AATGCAAAAA GGAGCGGAAG AAGAAAAAGA 900
98
99 AAGTGACCAA CATAATCTCA TTTGATGATG AGGAAGATGA GCAGAACTCT GGGGACGTGT 960

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101 TTAAAAAGAC ACCTGGGGCA GGGGAGAGCT CAGAGGACAA CTCCGACCGC TCCTCTGTCA 1020
102
103 ATATCATGTC CGCCTTTGAA AGCCCCCTTCG GGCCTAACTC CAATGGAATC AGAGCAGCAA 1080
104
105 CTCATGGAAA ATTGATTCCC TGTCTTTGAA CGGGGAGTTT GGGTACCAGA AGCTTGATGT 1140
106
107 GAAAAGCATC GATGATGAAG ATGTGGATGA AAACGAAGAT GACGTGTATG GAAACTCATC 1200
108
109 AGGAAGGAAG CACAGGGGCC ACTCGGAGTC GCCCGAGAAG CCACTGGAAG GGAACACCTG 1260
110
111 CCTCTCCCAG ATGCACAGCT GGGCTCCGCT GAAGGTGCTG CACAATGACT CCGACATCCT 1320
112
113 CTTCCCTGTC AGTGGCGTGG GCTCCTACAG CCCAGCAGAT GCCCCCCTCG GAAGCCTGGA 1380
114
115 GAACGGGACA GGACCAGAGG ACCACGTTCT CCCGGATCCT GGACTTCGGT ACAGTGTGGA 1440
116
117 AGCCAGCTCT CCAGGCCACG GAAGTCCTCT GAGCAGCCTG TTACTTCTGC CTCAGTGCCA 1500
118
119 GAGTCCATGA CAATTAGTGA ACTGCGCCAG GCCACTGTGG CCATGATGAA CAGGAAGGAT 1560
120
121 GAGCTGGAGG AGGAGAACAG ATCACTGCGA AACCTGCTCG ACGGTGAGAT GGAGCACTCA 1620
122
123 GCCGCGCTCC GGCAAGAGGT GGACACCTTG AAAAGGAAGG TGGCTGAACA GGAGGAGCGG 1680
124
125 CAGGGCATGA AGGTCCAGGC GCTGGCCAGC TATCTTTGCT ATTTTGTGAG GAGATTCTAA 1740
126
127 CCCCACGTGA GAACCATGTG GTGGAGAAAT GGAGGGAGAG AGAAATCCAA CAGTTCCTGA 1800
128
129 TAGTCTCATT TGAGCTCCTG GATCCAGTCT TTCCTGAAGC TGTGTTTCCT CTGGACTTTT 1860
130
131 CATGTATGTG AGCCAATAAA TTGCTTTCAT TCCTTGAAAA AAAAAA 1906
132

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Thr Gly Pro Gly Xaa Gly Xaa Met Ser Gly Ser Xaa Asn Xaa Asp
1 5 10 15
Lys Arg Gln Phe Leu Leu Glu Arg Leu Leu Asp Ala Val Lys Gln Cys
20 25 30
Gln Ile Arg Phe Xaa Gly Arg Lys Glu Ile Ala Ser Asp Ser Asp Ser
35 40 45

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153
154   Arg Val Thr Cys Leu Cys Ala Gln Phe Glu Ala Val Leu Gln His Gly
155           50                      55                      60
156
157   Leu Lys Arg Ser Arg Gly Leu Ala Leu Thr Ala Ala Ala Ile Lys Gln
158   65                      70                      75                      80
159
160   Ala Ala Gly Phe Ala Ser Lys Thr Glu Thr Glu Pro Val Phe Trp Tyr
161           85                      90                      95
162
163   Tyr Val Lys Glu Val Leu Asn Lys His Glu Leu Gln Arg Phe Tyr Ser
164           100                      105                      110
165
166   Leu Arg His Ile Ala Ser Asp Val Gly Arg Gly Arg Ala Trp Leu Arg
167           115                      120                      125
168
169   Cys Ala Leu Asn Glu His Ser Leu Glu Arg Tyr Leu His Met Leu Leu
170           130                      135                      140
171
172   Ala Asp Arg Cys Arg Leu Ser Thr Phe Tyr Glu Asp Trp Ser Phe Val
173   145                      150                      155                      160
174
175   Met Asp Glu Glu Arg Ser Ser Met Leu Pro Thr Met Ala Ala Gly Leu
176           165                      170                      175
177
178   Asn Ser Ile Leu Phe Ala Ile Asn Ile Asp Asn Lys Asp Leu Asn Gly
179           180                      185                      190
180
181   Gln Ser Lys Phe Ala Pro Thr Val Ser Asp Leu Leu Lys Glu Ser Thr
182           195                      200                      205
183
184   Gln Asn Val Thr Ser Leu Leu Lys Glu Ser Thr Gln Gly Val Ser Ser
185           210                      215                      220
186
187   Leu Phe Arg Glu Ile Thr Ala Ser Ser Ala Val Ser Ile Leu Ile Lys
188   225                      230                      235                      240
189
190   Pro Glu Gln Glu Thr Asp Pro Cys Leu Ser Cys Pro Gly Met Ser Val
191           245                      250                      255
192
193   Leu Met Pro Asn Ala Lys Arg Ser Gly Arg Arg Lys Arg Lys Xaa Pro
194           260                      265                      270
195
196   Thr Xaa Ser His Leu Met Met Arg Lys Met Ser Arg Thr Leu Gly Thr
197           275                      280                      285
198
199   Cys Leu Lys Arg His Leu Gly Gln Gly Arg Ala Gln Arg Thr Thr Pro
200           290                      295                      300
201
202   Thr Ala Pro Leu Ser Ile Ser Cys Pro Pro Leu Lys Ala Pro Ser Gly
203   305                      310                      315                      320
204
205   Leu Thr Pro Met Glu Ser Glu Gln Gln Leu Met Glu Asn Xaa Phe Pro

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206		325		330		335
207						
208	Val	Phe	Glu	Arg	Gly	Val
209				340		345
210						350
211	Arg	Xaa	Xaa	Arg	Cys	Gly
212				355		360
213						365
214	Ile	Arg	Lys	Glu	Ala	Gln
215				370		375
216						380
217	Gly	Arg	Glu	His	Leu	Pro
218					385	390
219						395
220	Gly	Ala	Ala	Gln	Xaa	Leu
221					405	410
222						415
223	Leu	Leu	Gln	Pro	Ser	Arg
224					420	425
225						430
226	Arg	Thr	Arg	Gly	Pro	Arg
227					435	440
228						445
229	Gly	Ser	Gln	Leu	Ser	Arg
230					450	455
231						460
232	Ser	Ala	Ser	Val	Pro	Glu
233					465	470
234						475
235	Thr	Val	Ala	Met	Met	Asn
236					485	490
237						495
238	Ser	Leu	Arg	Asn	Leu	Leu
239					500	505
240						510
241	Arg	Gln	Glu	Val	Asp	Thr
242					515	520
243						525
244	Arg	Gln	Gly	Met	Lys	Val
245					530	535
246						540
247	Val	Arg	Arg	Phe	Xaa	Pro
248					545	550
249						555
250	Gly	Arg	Glu	Lys	Ser	Asn
251					565	570
252						575
253	Ile	Gln	Ser	Phe	Leu	Lys
254					580	585
255						590
256	Glu	Pro	Ile	Asn	Cys	Phe
257					595	600
258						

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